

## **FIG.\_ 1A**

**SEQ ID NO: 1**

**Nucleotide Sequence Tankyrase Homologue isotype1**

CTTGAAAGACACTGGATTCATACTTTGCCTGGGTTATCTCTGTGTCTCACTACATAGACAAATA  
TTAGCTGTGAGCAGATCTTTTGTGCTTGTAGTCCCCCAGTTAGCAGAAACATTCTGTGAGA  
TAGATGTGGGAAAGGAATTCTAGCAAGAGTTGTCACTGTATCATAAGGTTGTGATTACATATTAA  
GTTTATACTTGAACATCTGAAAATGTATACATACTAAATATGCAGAACTCTATTGTAGAGTGAGAAA  
CATTGAACTTGAGCTTCAGTCACTTTTGTATTCTTCTTGAGGTTAGCAGTAGTACCAACCCA  
AGGCAC TGCTTAGGTACCTGCTGCTTAGTGGAGAGTCCCTGCGTTATCATTAAAGGTTGGCG  
GAAAGACGTAGTTGAATATTGCTTCAGAATGGTCAAGTGTCCAAGCACGTGATGATGGGGCCCTAT  
TCCTCTCATATGCATGCTCTTGGTCACTGCTGAAGTAGTCAATCTCCTTGCACATGGTGCAGA  
CCCCAATGCTCGAGATAATTGGAATTATACTCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGT  
TTGCATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATGGA  
TTTAGCAGATCCATCTGCCAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGC  
CAGGAGTGGCAATGAAGAAAAATGATGGCTACTCACACCATTAAATGTCAACTGCCACGCAAGTGA  
TGGCAGAAAGTCAACTCCATTACATTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTACT  
GCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGTACCATACACAATGCCTGTTCTA  
TGGTCATTATGAAGTAAGTAACTGAACTTTGGTCAAGCATGGCCTGTGTAATGCAATGGACTTGTGGCA  
ATTCACTCCTCTCATGAGGCAGCTCTAAGAACAGGGTTGAAGTATGTTCTCTCTTAAGTTATGG  
TGCAGACCCAACACTGCTCAATTGTCACAATAAAAGTGTCTAGACTGGCTCCCACACCACAGTTAA  
AGAAAGATTAGCATATGAATTAAAGGCCACTCGTTGCTGCAAGCTGCAAGGAGCTGATGTTACTCG  
AATCAAAAAACATCTCTCTGGAAATGGTGAATTCAAGCATCCTCAAACACATGAAACAGCATTGCA  
TTGTGCTGCTGCATCTCCATATCCAAAAGAAAGCAAATATGTGAACTGTTGCTAAGAAAAGGAGCAAA  
CATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGTGGCATCTGAGAAAGCTCATAATGATGT  
TGGTGAAGTAGTGGTGAACATGAAGCAAAGGTTAATGCTCTGGATAATCTGGTCAGACTCTACA

CAGAGCTGCATATTGTGGTCATCTACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACAT  
TATATCCCTCAGGGCTTACTGCTTACAGATGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGG  
TATCTCATTAGGTAAATTCAAGAGGCAGACAGACAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCGAAAC  
TGTAAAAAAACTGTGTACTGTCAGAGTGTCAACTGCAGAGACATTGAAGGGCGTCAGTCTACACCACT  
TCATTTGCAGCTGGGTATAACAGAGTGTCCGTGGAAATATCTGCTACAGCATGGAGCTGATGTGCA  
TGCTAAAGATAAAGGAGGCCTGTACCTTGACAAATGCATGTTCTATGGACATTATGAAGTTGCAGA  
ACTTCTGTTAACATGGAGCAGTAGTTAATGTAGCTGATTATGAAATTACACCTTACATGAAGC  
AGCAGCAAAAGGAAAATATGAAATTGCAAACCTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAAA  
CAGGGATGGAATACTCCTTGGATCTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGG  
AGATGCAGCTTGCTAGATGCTGCCAAGAAGGGTTGTTAGCCAGAGTGAAGAAGTTGTCTTCTCCTGA  
TAATGTAATTGCCGCGATAACCAAGGCAGACATTCAACACCTTACATTAGCAGCTGGTTATAATAA  
TTTAGAAGTTGCAGAGTATTGTTACAACACGGAGCTGATGTGAATGCCAAGACAAAGGAGGACTTAT  
TCCTTACATAATGCAGCATCTACGGGCATGTAGATGTAGCAGCTCTACTAATAAGTATAATGCATG  
TGTCAATGCCACGGACAAATGGGCTTACACCTTGCACGAAGCAGCCAAAGGGACGAACACAGCT  
TTGTGCTTGTGCTAGCCATGGAGCTGACCCGACTCTAAAAATCAGGAAGGACAAACACCTTAGA  
TTTAGTTTCAGCGGATGATGTCAGCGCTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTTTG  
TTACAAGCCTCAAGTGCCTAATGGTGTGAGAAGCCCAGGAGCCACTGCAGATGCTCTTCAGGTCC  
ATCTAGCCCATCAAGCCTTCTGCAGCCAGCAGCTTGACAACCTATCTGGAGTTTCAGAACTGTC  
TTCAGTAGTTAGTTCAAGTGGAACAGAGGGTGCTCCAGTTGGAGAAAAGGAGGTTCCAGGAGTAGA  
TTTAGCATAACTCAATTGTAAGGAATCTGGACTTGAGCACCTAATGGATATATTGAGAGAGAAC  
GATCACTTGGATGTATTAGTTGAGATGGGGCACAAGGAGCTGAAGGAGATTGAATCAATGCTTATGG  
ACATAGGCACAAACTAATTAAAGGAGTCGAGAGACTTATCTCCGGACAACAAGGTCTAACCCATATTT  
AACTTTGAACACCTCTGGTAGTGGAAACAATTCTTATAGATCTGTCCTGATGATAAAGAGTTTCAGTC  
TGTGGAGGAAGAGATGCAAAGTACAGTTGAGAGCACAGAGATGGAGGTATGCAGGTGGAATCTCAA  
CAGATACAATATTCTCAAGATTCAAGGTTGTAACAAGAAACTATGGAAAGATAACACTCACCGGAG  
AAAAGAAGTTCTGAAGAAAACCACAACCATGCCAATGAACGAATGCTATTCTATGGGTCTCCTTGT  
GAATGCAATTATCCACAAAGGCTTGATGAAAGGCATGCGTACATAGGTGTATTTGGAGGAGGTACTGGGTGTCC  
AGTTCACAAAGACAGATCTGTTACATTGCCACAGGCAGCTGCTCTTGCCTGGTAACCTGGAAA  
GTCTTCTGCAGTTGCAATGAAAATGGCACATTCTCCTCCAGGTATCACTCAGTCAGTCACTGGTAG  
GCCCAAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACAGGCTTATCCTGAGTA  
TTAATTACTTACCAAGATTATGAGGCCTGAAGGTATGGTCATGGATAAATAGTTATTTAAGAAACTA  
ATTCCACTGAACCTAAATCATCAAAGCAGCAGTGGCCTACGTTACTCCTTGCTGAAAAAA  
AA

## **FIG.\_ 1B**

## **FIG.\_2A**

**SEQ ID NO: 2**

**Nucleotide Sequence Tankyrase Homologue isotype2**

CGCGCTGCCGCCGCCGGGGCAGCCGGGGCAGGGAGCCCAGCGAGGGCGCGCGTGGCGCG  
CCCATGGGACTGCGCCGGATCCGGTGACAGCAGGGAGCCAAGCGGCCGGGCCCTGAGCGCGTCTCTC  
CGGGGGCCTCGCCCTCTGCTCGCGGGCCGGGCTCTGCTCCGGTGTGGCGCTGGCTGGCTG  
TGGCGCGGCCAGGATCATGTCGGGTCGCCGCTGCCGGGGAGCGGCCTGCGGAGCGCCGG  
CCGAGGCCGTGGAGGCCGGCCGAGAGCTGTTGAGGGCGTCCGCAACGGGACGTGGAACGAGTCA  
AGAGGCCTGGTACGCCCTGAGAAGGTGAACAGCCGACACGGGGCAGGAATCCACCCGCTGCACT  
TCGCCGCAGGTTGGCGAAAGACGTAGTTGAATATTGCTTCAGAATGGTCAAATGTCCAAGCAC  
GTGATGATGGGGCCTATTCTCTTCAATGCATGCTCTTGGTATGCTGAAGTAGTCAATCTCC  
TTTGCGACATGGCAGACCCCAATGCTGAGATAATTGAAATTACTCCCTCCATGAAGCTGCAA  
TTAAAGGAAAGATTGATGTTGCATTGTGCTGTTACAGCATGGAGCTGAGCCAACCCTCGAAATACAG  
ATGGAAGGACAGCATTGGATTAGCAGATCCATGCCAAAGCAGTGTTACTGGTGAATATAAGAAAG  
ATGAACCTTAGAAAGTCCAGGAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCAATTAAATG  
TCAACTGCCACGCAAGTGAATGGCAGAAAGTCAACTCCATTACATTGGCAGCAGGATATAACAGAGTAA  
AGATTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGTACCAT  
TACACAATGCCCTTTATGGTCAATTGAAGTAATGAACTTTGGTCAAGCATGGCCTGTGAA  
ATGCAATGGACTTGTGGCAATTCACTCCCTTCACTGAGGGCAGCTCTAAGAACAGGGTTGAAGTATGTT  
CTCTCTCTTAAGTTATGGCAGACCCAACACTGCTCAATTGTACAATAAAAGTGTATAGACTTGG  
CTCCCACACCAGTTAAAGAAAGATTAGCATATGAATTAAAGGCCACTCGTTGCTGCAAGCTGCAC  
GAGAAGCTGATGTTACTCGAATAAAAACATCTCTGGAAATGGTGAATTCAAGCATCCTCAAA  
CACATGAAACAGCATTGCATTGTGCTGCATCTCCATATCCAAAAGAAAGCAAATATGTGAACGT  
TGCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTGACTCCTCTGCACGTGGCATCTG  
AGAAAGCTCATAATGATGTTGAAGTAGTGGTAAACATGAAGCAAAGGTTAATGCTCTGGATAATC

TTGGTCAGACTTCTACACAGAGCTGCATATGTGGTCATCTACAAACCTGCCGCCTACTCCTGAGCT  
ATGGGGTGTGATCCTAACATTATATCCCTCAGGGCTTACTGCTTACAGATGGAAATGAAAATGTAC  
AGCAACTCCTCCAAGAGGGTATCTCATTAGTAATTAGGACAGAGACAGACAATTGCTGGAAGCTGAA  
AGGCTGGAGATGTCGAAACTGTAAAAAAACTGTGTACTGTTAGAGTGTCAACTGCAGAGACATTGAAG  
GGCGTCAGTCTACACCACTCATTGAGCTGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCTAC  
AGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTGTACCTTGACAATGCATGTTCTATG  
GACATTATGAAGTTGAGACTTCTTAAACATGGAGCAGTAGTTAATGTAGCTGATTATGGAAAT  
TTACACCTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTGCAAACCTCTGCTCCAGCATGGT  
CAGACCCCTACCAAAAAAAACAGGGATGAAATACTCCTTGGATCTGTTAAAGATGGAGATAAGATA  
TTCAAGATCTGCTTAGGGGAGATGAGCTTGTAGATGCTGCCAAGAAGGGTTGTTAGCCAGAGTGA  
AGAAGTTGTCTCTCCTGATAATGTAATTGCGCGATAACCAAGGCAGACATTCAACACCTTACATT  
TAGCAGCTGGTTATAATAATTAGAAGTTGAGCTGAGTATTGTTACAACACGGAGCTGATGTGAATGCC  
AAGACAAAGGAGGACTTATCCTTACATAATGAGCTTACGGGATGCTAGATGTAGCAGCTCTAC  
TAATAAAGTATAATGCATGTGCAATGCCACGGACAAATGGCTTACACCTTGACAGCAGGCC  
AAAAGGGACGAACACAGCTTGTGCTTGTGCTAGCCCATGGAGCTGACCCACTCTAAAAATCAGG  
AAGGACAAACACCTTGTAGATTAGTTGCTAGCAGGATGTCAGCGCTCTGACAGCAGCCATGCC  
CATCTGCTCTGCCCTTTGTTACAAGCCTCAAGTGTCAATGGTGAGAAGGCCAGGAGCCACTGCAG  
ATGCTCTCTTCAGGTCCATCTAGCCCATCAAGCCTTCTGCAGCCAGCAGTCTGACAACCTATCTG  
GGAGTTTCAGAACTGTCTCAGTAGTTAGTTGCTAGCAGGATGTCAGCGCTCTGACAGCAGCCATGCC  
AGGAGGTTCCAGGAGTAGATTAGCTAACTCAATTGTAAGGAATCTGGACTTGAGCACCTAATGG  
ATATATTGAGAGAGAACAGATCACTTGGATGTTAGTTGAGATGGGCACAAGGAGCTGAAGGAGA  
TTGGAATCAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTCAGAGAGACTTATCTCCGGACAAC  
AAGGTCTAACCCATATTTAACCTTGAACACCTCTGGTAGTGGAAACAATTCTTATAGATCTGCTCTG  
ATGATAAAGAGTTCAGTCTGTGGAGGAAGAGATGCAAAGTACAGTTGAGAGCACAGAGATGGAGGTC  
ATGCAGGTGGAATCTCAACAGATAAACTTCAAGATTGAGCTGAAAGGTTGTAACAAGAAACTATGGG  
AAAGATAACACTCACCGGAGAAAAGAAGTTCTGAAGAAAACCACAACCATGCCAATGAACGAATGCTAT  
TTCATGGGTCTCTTGTGAATGCAATTATCCACAAAGGCTTGTGAAAGGCATGCGTACATAGGTG  
GTATGTTGGAGCTGGCATTATTTGCTGAAAACCTTCCAAAGCAATCAATATGTATATGGAATTG  
GAGGAGGTACTGGGTGTCAGTCACAAAGACAGATCTTGTACATTGCCACAGGAGCTGCTCTT  
GCCGGGTAACCTGGAAAGTCTTCCGTGAGTCAGTGCATGAAATGGCACATTCTCCAGGTC  
ATCACTCAGTCAGTGTAGGCCAGTGTAAATGCCCTAGCATTAGCTGAATATGTTATTACAGAGGAG  
AACAGGCTTATCCTGAGTATTAATTACTTACAGATTATGAGGCCTGAAGGTATGGTCATGGATAAA  
TAGTTATTTAAGAAACTAATTCCACTGAACCTAAATCATCAAAGCAGCAGTGGCCTACGTTTAC  
TCCTTGCTGAAAAAA

## FIG.\_2B

**SEQ ID NO: 3**

**Amino Acid Sequence Tankyrase Homologue isotype1**

GFGRKDVEYLLQNGASVQARDDGGIPLHNACSGHAEVVNLLRHGADPNARDNWNYTPLHEAAIKG  
KIDVCIVLLQHGAEPITIRNTDGRTALDLADPSAKAVLTGEYKKDELLESARSGNEEKMALLTPLNVNC  
HASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAM  
DLWQFTPPLHEAASKNRVEVCSLLLSYGADPTLLNCHNKSAILDAPTPQLKERLAYEFKGHSLLQAAREA  
DVTRIKKHLSEMVNFHPQTHETALHCAAASPYPKRKQICELLRKGANINEKTKEFLTPLHVASEKA  
HNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQL  
LQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHG  
ADVHAKDKGGLVPLHNACSYGHYEVAAELLVKHGAVVNADLWKFTPLHEAAAKGKYEICKLLLQHGADP  
TKKNRDGNTPLDLVKDGDTIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHAA  
GYNNEVAEYLLQHGADVNAQDKGGIPLHNAAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKG  
RTQLCALLLAHGADPTLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADAL  
SSGPSSPSSLSAASSLDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDF  
EREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVVERLISGQQGLNPYLTINTSGSGTILIDLSPDDK  
EFQSVEEEMQSTVREHRDGGHAGGI FNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHG  
SPFVNAAIHKGDERHAYIGGMFGAGIYFAENSSKSNQYVYIGGGTGCVPVKDRSCYICHRLQLFCRV  
TLGKSFLQFSAMKMAHSPPGHHSVTGRPSVNGLALAELYRGEQAYPEYLITYQIMRPEGMVDG

**FIG.\_3**

**SEQ ID NO: 4**

**Amino Acid Sequence Tankyrase Homologue isotype2**

RCSARRGAAGGQGAQRGARVGAAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLALLAV  
AAARIMSGRRCAAGGAACASAAAEEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHF  
AAGFGRKDVVEYLLQNGANVQARDDGLIPLHNACSFHAEVVNLLRHGADPNARDNWNYTPLHEAAI  
KGKIDVCIVLLQHGAEPITRNTDGRITALDADPSAKAVLTGEYKKDELLESARSGNEEKMALLTPLNV  
NCHASDGRKSTPLHLAGYNRVKIVQLLLQHGAADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVN  
AMDLWQFTPPLHEAASKNRVEVCSLLSYGADPTLLNCHNKSAILDAPTPQLKERLAYEFKGHSLLQAAR  
EADVTRIKKHSLEMVNFHKPQTHETALHCAAASPYPKRQICELLRKGANINEKTKEFLTPLHVASE  
KAHNDVVEVVVKHEAKVNALDNLGQTSIHRAAYCGHLQTCRLLSYGCDPNIISLQGFTALQMGNEVQ  
QLLQEGLSLGNSEADRQLLEAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVEYLLQ  
HGADVHAKDKGGLVPLHNACSYGHYEVALLVKHGAVNVADLWKFPLHEAAAKGKYEICKLLLQHGA  
DPTKKNRDGNTPLDLVKDGTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHL  
AAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAAASYGHVDVAALLIKYNACVNATDKWAFTPPLHEAAQ  
KGRTQLCALLLAHGADPTLKNQEGQTPLDVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATAD  
ALSSGPSSPSSLSAASSLDNLGSFSSELSSVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM  
IFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVVERLISGQQGLNPYLTNTSGSGTILIDLSPD  
DKEFQSVEEEMQSTVREHRDGGHAGGI FNRYNILKIQKVCNKKLWERYTHRKEVSEENHNHANERMLF  
HGSPFVNAAIHKGFDERHAYIGGMFGAGIYFAENSSKSNSQYVYGGGTGCPVHKDRSCYICHRLFC  
RVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG

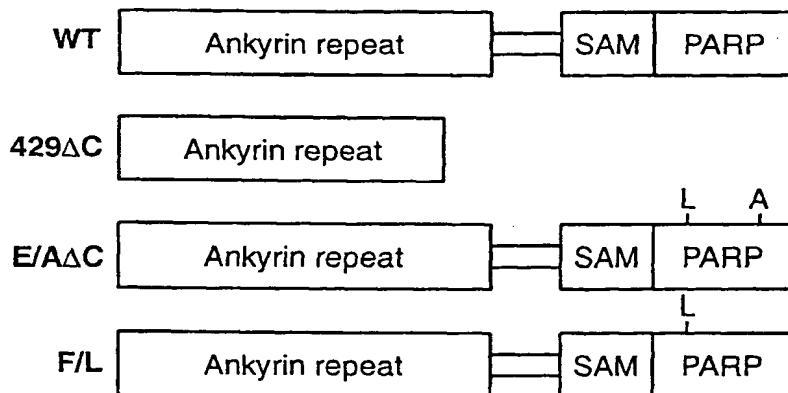
**FIG.\_4**

### Schematic Presentation of Dominant Negative Mutants for Tankyrase Homologue

#### Dominant Negative Mutants

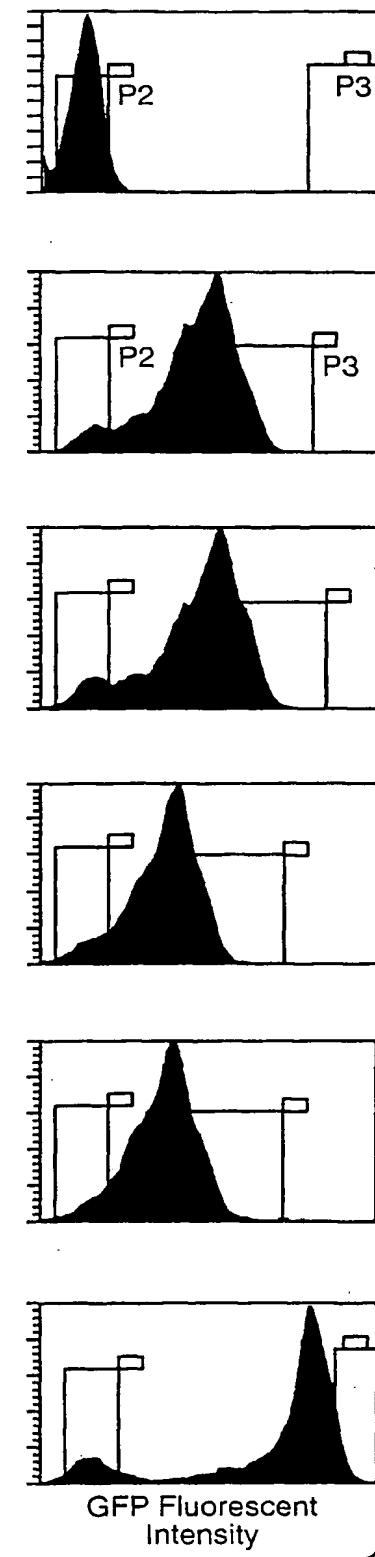
Truncation: 429 $\Delta$ C- of the C-terminal catalytic domain – truncation of the catalytic domain of PARP acts as a dominant negative when overexpressed *in vivo* (Oncogene 1999 Nov 25; 18(50):7010-5)

Point mutant: E945A $\Delta$ C- conserved residue in PARP domain, thought to be important in NAD<sup>+</sup> binding

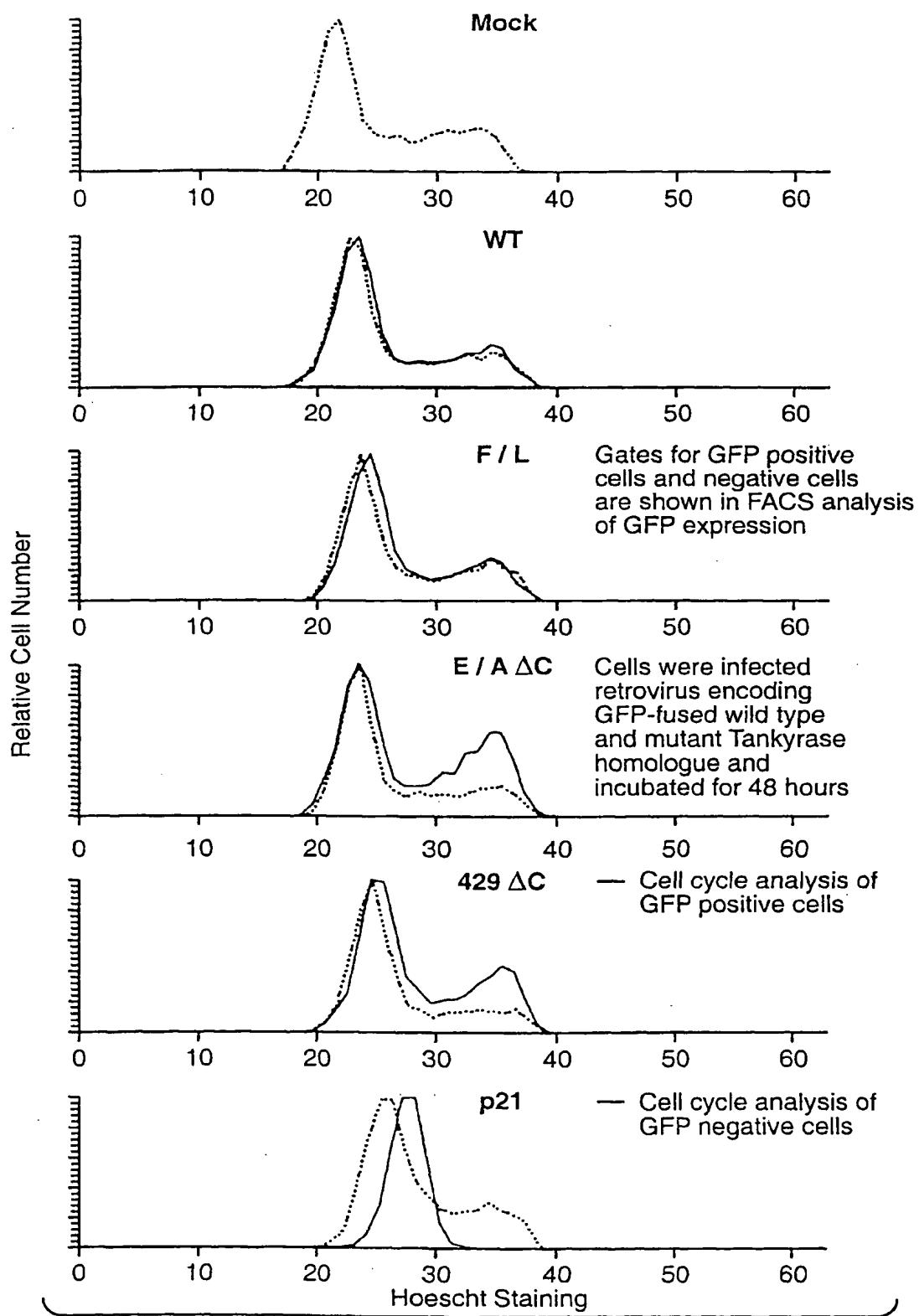


**FIG.\_5**

**Cell Cycle Analysis of A549 Cells  
Infected With GFP-fused Wild Type  
and Mutant Tankyrase Homologue**

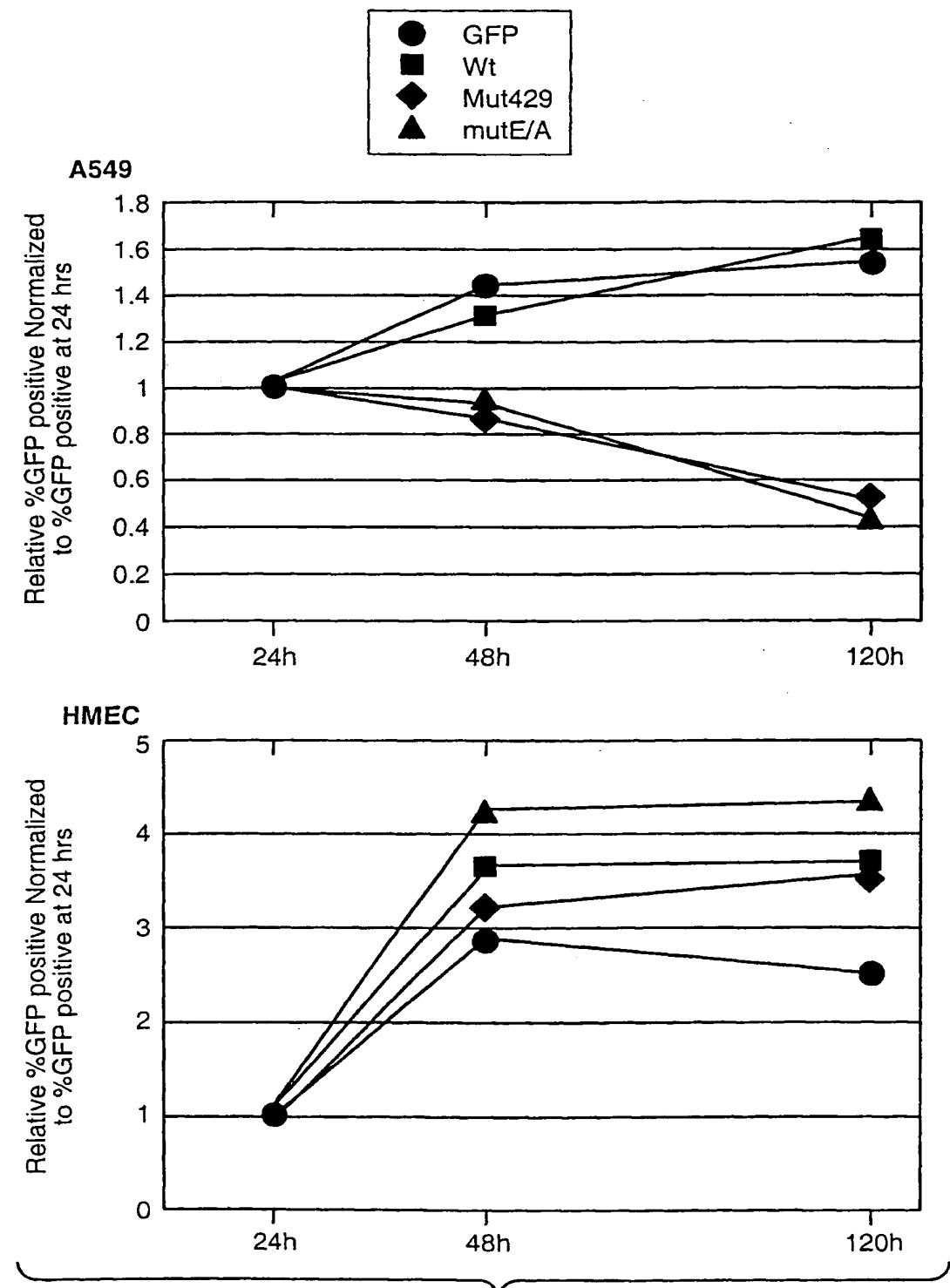


**FIG.\_6A**



**FIG. 6B**

**Kinetics of GFP Positive cells in A549 Cells and Human Mammary Epithelial Cells (HMEC) After Retrovirus Infection Encoding GFP-fused Wild Type and Mutant Tankyrase Homologue**



**FIG. 7**

## The Binding Site of Antisense Oligos Against Tankyrass Homologue

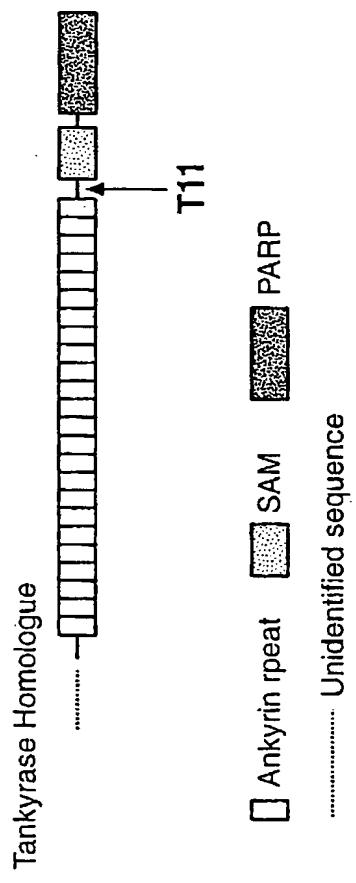
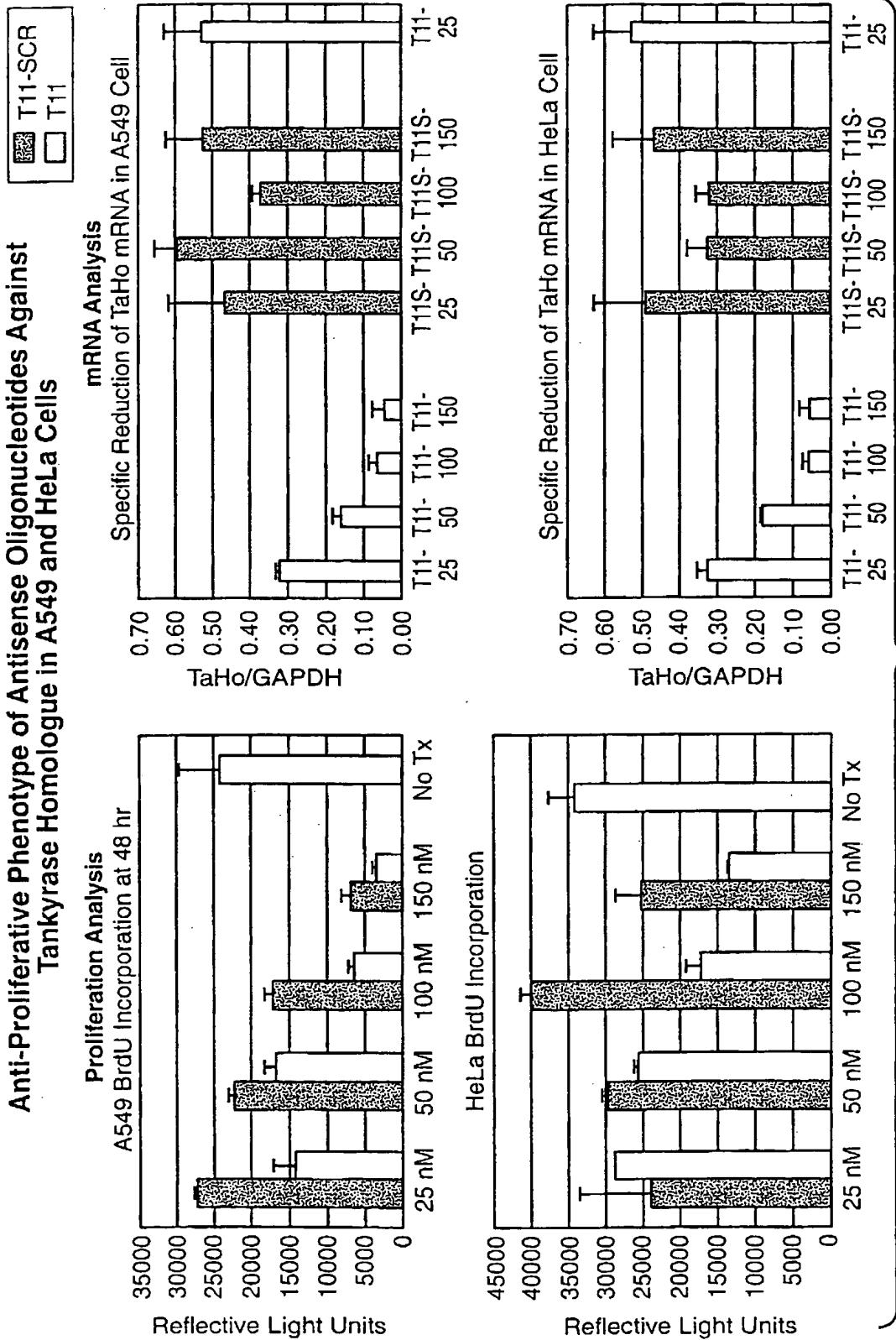


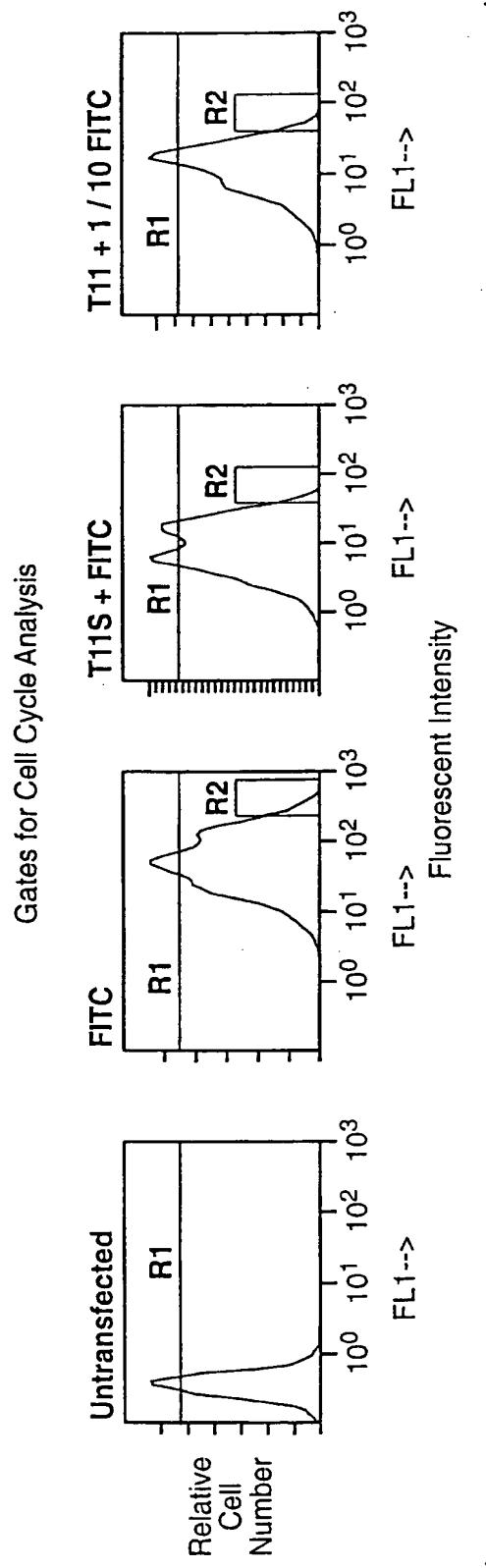
FIG. 8

**Anti-Proliferative Phenotype of Antisense Oligonucleotides Against  
Tankyrase Homologue in A549 and HeLa Cells**



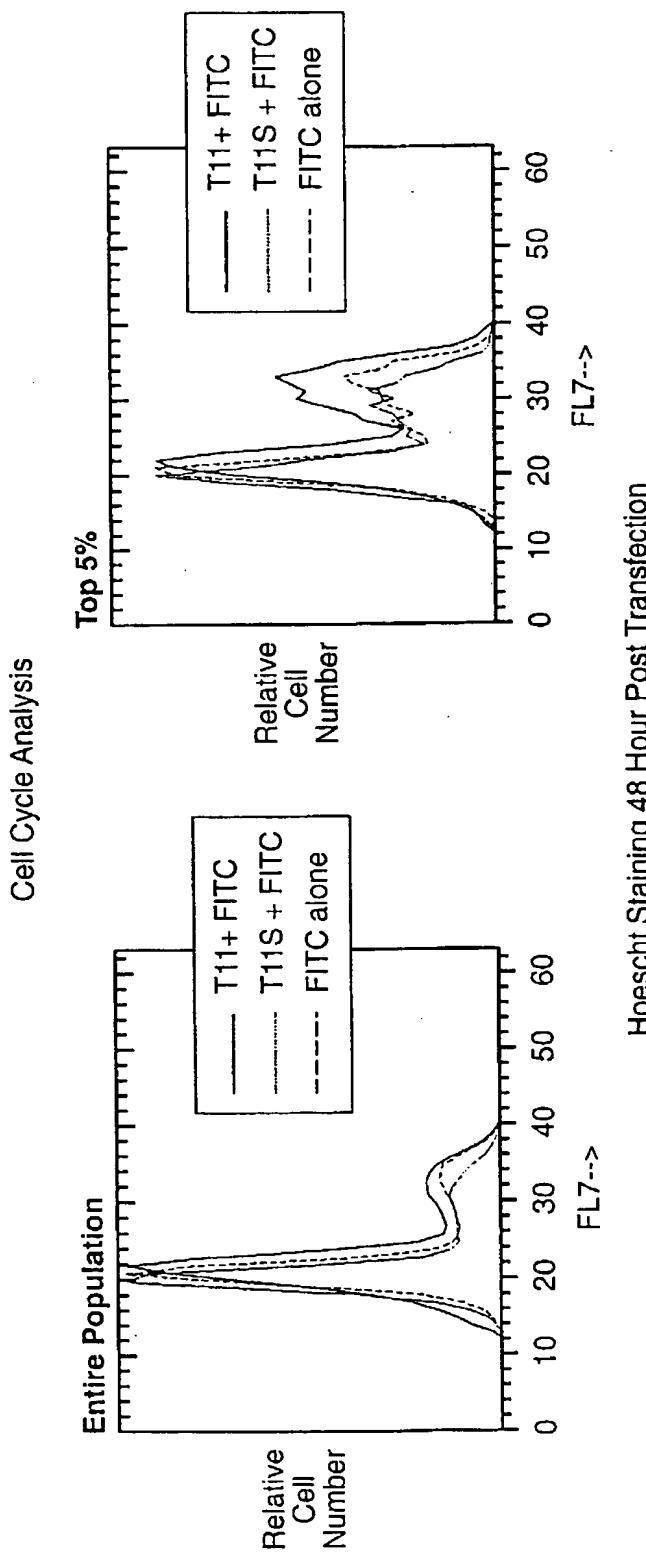
**FIG. 9**

**Cell Cycle Analysis of A549 Cells Transfected with Antisense Oligonucleotides Against Tankyrase Homologue at 48 Hours, Antisense Oligonucleotides (T11) and Control Oligonucleotides (T11S) were transfected with FITC-labeled random 20mer Oligonucleotides (FITC), After 48 Hours, entire population (R1) and Top 5% (R2) of FITC transfected cells were analyzed for cell cycle**



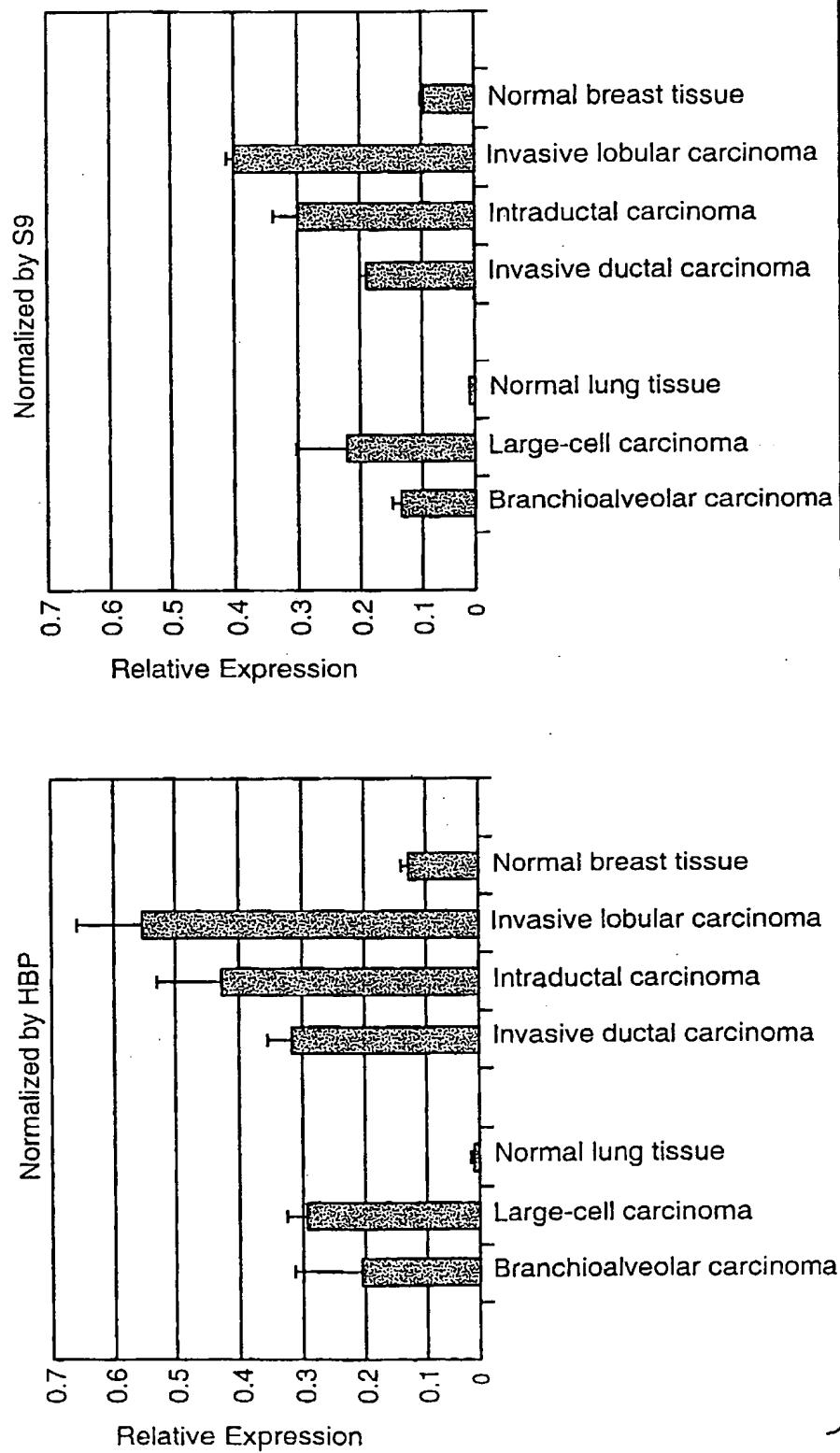
**FIG. 10A**

**Cell Cycle Analysis of A549 Cells Transfected with Antisense Oligonucleotides Against Tankyrase Homologue at 48 Hours, Antisense Oligonucleotides (T11) and Control Oligonucleotides (T11S) were transfected with FITC-labeled random 20mer Oligonucleotides (FITC), After 48 Hours, entire population (R1) and Top 5% (R2) of FITC transfected cells were analyzed for cell cycle**



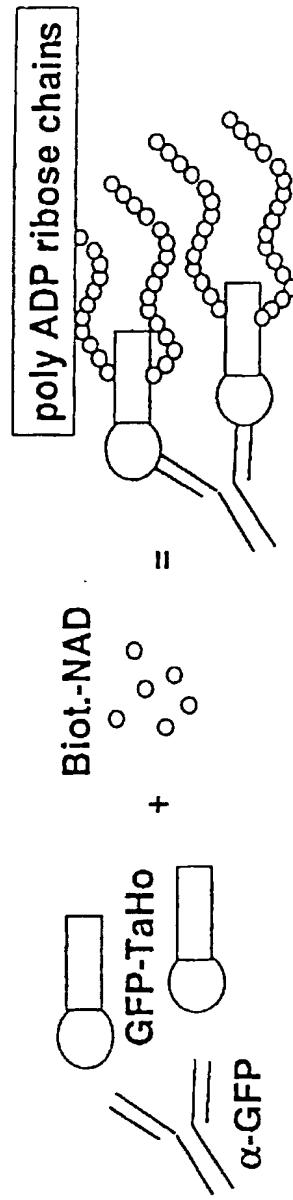
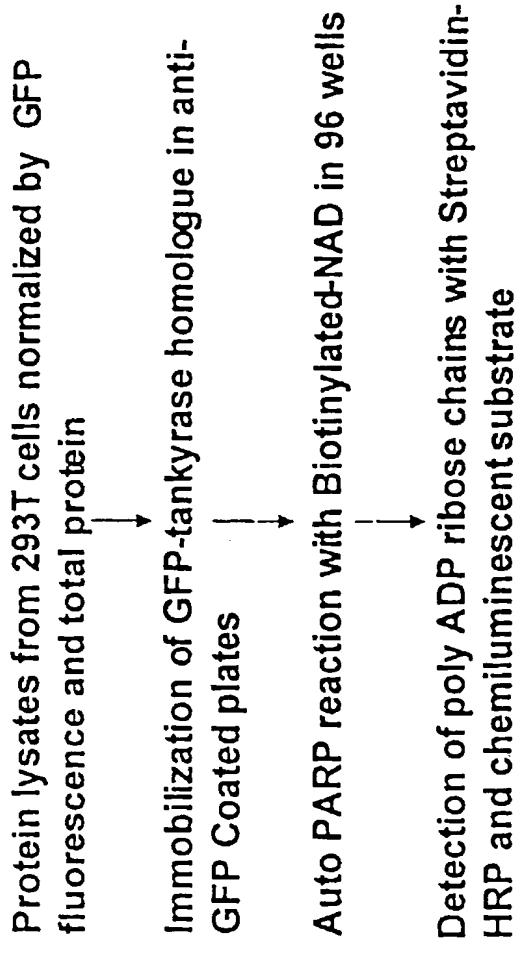
**FIG. - 10B**

**mRNA Expression of Tankyrase Homologue in Several Tumors and Normal Tissues by a Taqman Analysis, mRNA Expression was Normalized by 90kDa Highly Basic Protein (HBP) and Ribosomal Protein S9 (S9)**



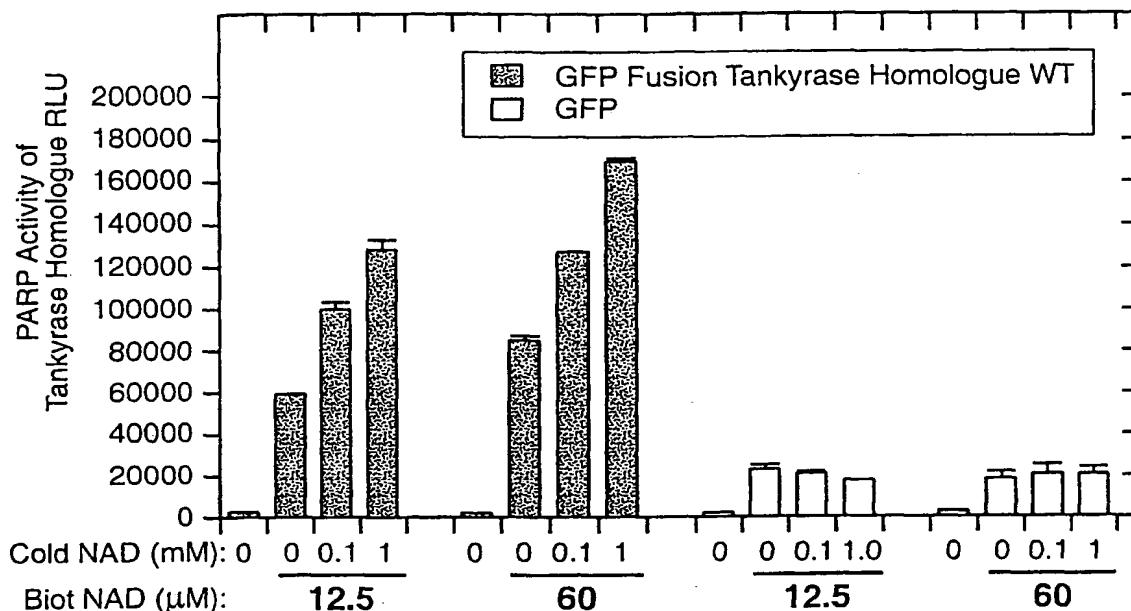
**FIG.- 11**

Procedure for Nonisotopic Detection of Poly-ADP Ribosylation  
Using Anti-GFP mAb-Coated Plates



**FIG. 12**

**Non-Isotopic Plate-Based Detection of TaHo PARP Activity in the Presence of Biotinylated NAD**



**FIG.\_ 13**

**Comparison of IC<sub>50</sub> Values of the PARP Inhibitors**

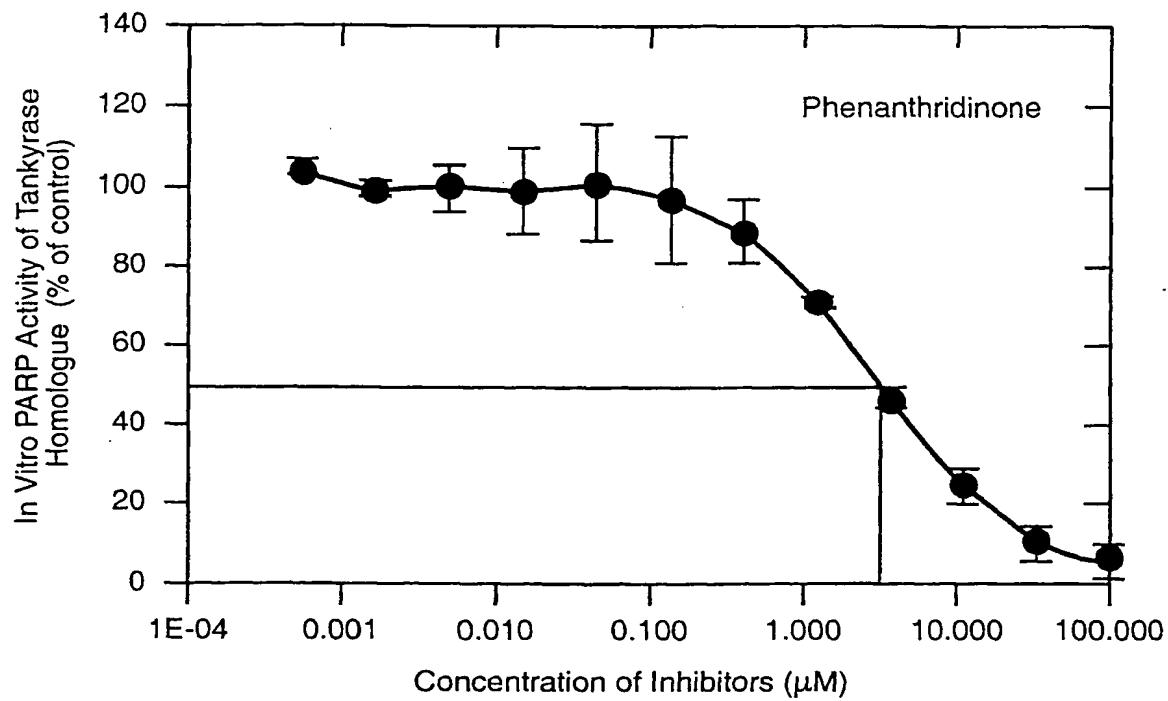
	Approximate IC <sub>50</sub> (nM)		hPARP assay IC <sub>50</sub> (nM)		
	TaHo		Rigel	Decker*	Rankin*
3AB	>50 000		5 000	2 000	5 400
6(5H)Phenanthridinone	1 000-2 000		300		
Niacinamide	>50 000		30 000	>>5 000	31 000

\* Decker P et al., Clinical Cancer Research. 1999 May; 5:1169-1172

\* Rawkin PW et al., J Biol Chem. 1989 Mar 15;264(8):4312-4317

**FIG.\_ 14**

**Inhibition of Tankyrase Homologue PARP Activity  
by hPARP Inhibitors**



**FIG.\_ 15**

**TH-1: Tankyrase Homologue isoform-1, TH-2: Tankyrase Homologue isoform-2**  
**M (Red): the first methionine in the sequence, Z: stop codon**  
**In this figure, the first methionine in TH-1 sequence is position 1 (iii)**

## FIG.-16A

Taho C terminus deletion mutant ends at position 429 (K) and adds 28 amino acids because of frame shift.

Taho F/L mutant has the mutation at position 871

Taho E/A dc mutant has the mutation at position 948, ends at position 957 (A) and adds 2 amino acids.

TH-1	-----	RCSARRGAAGGQGAQORGARVGAAGTAPDPVTAGSQ	-231
TH-2	-----		
TH-1	-----	AARALSASSPGLALLLAGPGLLRLLLAVAAARIMSGRRCAAGGAAACASAEEAVE	-171
TH-2	-----		
TH-1	-----	PAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVEYLLQNGA	-111
TH-2	-----		
	-----	Ankyrin repeat	
	-----	Ankyrin repeat	
TH-1	-----	SVQARDGGGLIPLHNACSEGHAEVVNLILRHGADPNARDNWNNTPLHEAAIKGKIDVCIV	-51
TH-2	-----	NVQARDGGGLIPLHNACSEGHAEVVNLILRHGADPNARDNWNNTPLHEAAIKGKIDVCIV	-51
	-----	Ankyrin repeat	
TH-1	-----	LLQHGAEPITRNTDGRNTADPSAKAVLTGEYKKDELLESARSQNEEKMMALLTPINV	10
TH-2	-----	LLQHGAEPITRNTDGRNTADPSAKAVLTGEYKKDELLESARSQNEEKMMALLTPINV	10
	-----	Ankyrin repeat	
	-----	• TH1 start	

## FIG.- 16B

		Ankyrin repeat	Ankyrin repeat	
TH-1		NCHASDGRKSTPLHLAAGYNRVRKVIVQLLLQHGA DVHAKDKGDLYPLHNACSYGHYEVTTEL		70
TH-2		NCHASDGRKSTPLHLAAGYNRVRKVIVQLLLQHGA DVHAKDKGDLYPLHNACSYGHYEVTTEL		70
		Ankyrin repeat	Ankyrin repeat	
TH-1		LVKHGACVNAMDLWQFTPPLHEAASKNRVECSLL SYGADPTLLNCHNKSAILDAPTPQL		130
TH-2		LV		
		Ankyrin repeat	Ankyrin repeat	
TH-1		KERLAYEFKGHSLLQAAREADVTRIKKHL SLEMVNFKHPOTHETALHCAASPYPKRKQI		190
		Ankyrin repeat	Ankyrin repeat	
TH-1		CELLLRKGANINEKTKREFLTPLH VASEKAHNDVVEVVVKHEAVYNALDNLGQTSLH RAY		250
		Ankyrin repeat	Ankyrin repeat	
TH-1		CGHLQTCRLLLSYGC DPNIISLQGFTALQMG NENVQQLLQEGISLG NSEADRLQLEAKA		310
		Ankyrin repeat	Ankyrin repeat	
TH-1		GDVETVKKLCTVQSVNCRDIEGRQSTPLH FAAGYNRSVVEYLLQHGA DVHAKDKGGLVP		370
		Ankyrin repeat	Ankyrin repeat	
TH-1		LHNACSYGHYEVAELLV KHGAVVNADLW KFTPLHEAAAKG KYEICKLLLQH GADPTKKN		T 430
		Ankyrin repeat	Ankyrin repeat	Deletion--•
TH-1		GMEILLWILLK MEOIQIFKICL GEMQLCZ RDGNTPLDLY KDGDTDIQD LLRGDA LLDAKKGCL ARVKKLSSPD NVNCRDTQGR HSTP		490
		Ankyrin repeat	Ankyrin repeat	

## FIG.- 16C

TH-1                    LHLAAGYNNLEVAEYLLQHGA  
                          DNAQDKGGGLIPLHNAASYGHVDVA  
                          ALLIKYNACVNATD 550  
                          Ankyrin repeat                    Ankyrin repeat

TH-1                    KWAFTPLHEAAQKGR  
                          TQLCALLLAHGA  
                          DPTLKNQEGQTPLDI  
                          VSADDVSALLTAAMPPSA 610  
                          Ankyrin repeat                    Ankyrin repeat

TH-1                    LPSCYKPQVLNGVRSPG  
                          ATADALSSGPSSSL  
                          SAASSLDNL  
                          SGSFSELSSV  
                          VSSSGT  
                          EG 670  
                          Ankyrin repeat                    Ankyrin repeat

TH-1                    ASSLEKKE--VPGVDF  
                          PSITQFV  
                          VRNLGLEH  
                          LMDIFERE  
                          QITLDV  
                          LVM  
                          GMGH  
                          KELKEIG  
                          INAY 730  
                          SAM domain

TH-1                    GHRHKLIK  
                          GVERLISGQQGL  
                          NPYLT  
                          LNTSGSGT  
                          ILIDLS  
                          PDDKEF  
                          QOSV  
                          EEMQ  
                          STV  
                          REHR 790

TH-1                    DGGHAGGI  
                          FNRYN  
                          NILKIQ  
                          KV  
                          CN  
                          KKL  
                          WERYT  
                          HRR  
                          KEV  
                          SEEN  
                          HNH  
                          ANER  
                          MFL  
                          FH  
                          GSP  
                          FVN  
                          NAI  
                          I 850

TH-1                    HKGFDERHAY  
                          IGGMF  
                          GAGIY  
                          FAENSS  
                          KSQVY  
                          VIGGGT  
                          GCPV  
                          HKDR  
                          SCYICH  
                          RQLL  
                          FCR 910  
                          F → L mutation  
                          PARP domain

TH-1                    VTLGKSFLQFSAMKMAH  
                          SPPGHHSVT  
                          GRPSVNGL  
                          ALAEV  
                          YIYGEQAY  
                          PEYLTYQIMRP 970  
                          • E → A                    • Deletion.

TH-1                    EGMV  
                          DG 976